

31 ATGGCCAACAAGCTGAGGAAATCGAACGCCATCGAATGGGCCACGGCCACCGGCACAGTACCGCTCCTGGAAAGGAGCTGCTGCCACAGC
 1 M A N K L R R S N A I E W A T A T G T V P L L E R S C C H S

91 GAGGACGCCGCACTGGAGCCCCAAGCGAGCAAAACCAGCCATAGAGAACAAGCCCCATCCTGCGCCACCTGAGCCAACTGAGCCACCTG TM
 31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L

181 CTCATCATCGCCGGACTGCTGATCGTCTGCTTGGCGGGCGTGACGAGGGCGCGCGGCATGCGCGCTCATGTTGAGGAGTCCGACACG
 61 L I I A G L L I V C L A G V T E G R R H A P L M F E E S D T

271 GGCAGGCGGTCCAACCGACGCGGTACCGAATCCAGTCTGGCAAGTTTGGCGCAATTGGGGTCCACCTGGTATGCGGATTGGGT
 91 G R R S N R P A V T E C Q E G K V L R E L G S T W Y A D L G

361 CCACCCITCGGAGTTATGTACTGCATCAAGTGTGAATGTGTCGCAATACCCAAGAAGCGGCGCATCGTTGCACGCGTCCAGTGTCCGAAT
 121 P P F G V M Y C I K C E C V A I P K K R R I V A R V Q C R N } CRI

451 ATCAAAAACAGTGCCTCGCGCGGCAAAATGCGATGATCCCATCTCGTTSCCGGAAAATGCTGCAAGACCTGTCCCGGCGATCGAAACGAT
 151 I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D

541 ACGGATGTAGCCTTGGATGTGCCCGTGCCTCAATGAAGAGGAAGAGCGCAACATGAACATTACGCTGCGTTGCTAACGGGCGCACCTCC
 181 T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S

631 TATTTCTCAAGGGTGAAGAAATGAAGTCCATGTACACCACCTACAATCCGCAGAATCTGCTGGCCACCGCCCGTTTCCTGTTCCACAAG
 211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K

721 AAGAATCTATACTACTCTTCTACACCTCATCGGAATCGGTCTCCCGTGCCATTCAATTCGTGATGATGCGGGTGTAACTCCTGGAG
 241 K N L Y Y S F Y T S S R I G R P R A I Q F V D R A G V I L E

811 GAGCATCAACTGGAGACCCTTGGCGGGCACTCTCAGTGTCTATCAGAATGCCACGGGCAAGATCTGA
 271 E H Q L E T T L A G T L S V Y A N A T G K I STOP

FIGURE 1

1 ATGGCCAAACAAGCTGAGGAAATCGAACGCCATCGAATGGGCCACGGCCACGGGCACAGTACCGCTCCTGGAAAGGAGCTGCTGCCACAGC
 1 M A N R L R K S N A I E W A T A T G T V P L L E R S C C H S
 91 GAGGACGCCGCACTGGAGCCCCAAGCGAGCAAAACAGCCATAGAGAAACAGCCCCATCCTGCGCCACCTGAGCCAACTGAGCCACCTG TM
 31 E D A A L E P Q A S K T S H R E Q A P I L R , H L S , Q L S H L
 181 CTCATCATCGCCGACTGCTGATCGTCTGCTTGGCGGGCGTGACGGAGGGCCGCCGCGCATGCGCCGCTCATGTTGAGGAGTCCGACAGC
 61 L I I A G L L I V C L A G V T E G R R H A P L M F E E S D T
 271 GGCAGGCGGTCCAACCGACCGCGGTACCGAATGCCAGTTTGGCAAAGTTTGGCGGAATTGGGGTCCACCTGGTATGCGGATTGGGT
 91 G R R S N R P A V T E C Q F G K V L R E L G S T W , A D L G
 361 CCACCCTTCGGAGTTATGTACTGCATCAAGTGTGAATGTGTGCGCATACCAAGAAGCGGCGCATCGTTGCACGCGTCCAGTGTGCAAT
 121 P P F G V M Y C I K C E C V A I P K K R R I V A R V Q C R N } CRI
 451 ATCAAAAACGAGTGGCCGCGGCAAAATGCCGATGATCCGATCTCGTTGCCCGGAAAATGCTGCAAGACCTGTCCCGGCGATCGAAACGAT
 152 I K N E C P P A K C D D P I S L P G K C C K T C P G D E N D
 541 ACGGATGTAGCCTTGGATGTGCCCGTGCCCAATGAAGAGGAAGACCGCAACATGAAACATTACGCTGCGTTGCTAACGGGCGCACCTCC
 181 T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S
 631 TATTTCTCAAGGCTGAGGAAATGAAGTCCATGTACACCACCTACAATCCGAGAATCTGGTGGCCACCGCCCGTTTCTGTTCACAAG
 211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K
 721 AAGAATCTATACTACTCTTCTACACCTCATCGCGAATCGGTGTCGCGGTGCCATTCAATTCGTTGATGATGCGGGTGAATCCTGGAG
 241 K N L Y Y S F Y T S S R I G R P R A I O F V D D A G V I L E
 811 GAGCATCAACTGGAGACCACCTTGGCGGGCACTCTCAGTGTCTATCAGAATGCCACGGGCAAGATCGGCCGCGGCTCGAGGGTACCTCTA
 271 E H Q L E T T L A G T L S V Y A N A T G K I G R G S R V P L } pUAS
 901 GAGGATCTTTCTGAAGGAACCTTACTTCTGTCTGTGACATAATTGGACAACTACCTACAGAGATTAAAGCTCTAA
 301 E D L C E G T L L L W C D I I C N T T Y R D L K L STOP } Sequences

FIGURE 2

C cont'd

1 ATGGCCAACAAGCTGAGGAAATCGAACGCCATCGAATGGGCCACGGCCACCGGCACAGTACCGCTCCTGGAAAGGAGCTGCTGCCACAGC
 1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S
 91 GAGGACCCGCACTGGAGCCCAAGCGAGCAAAACCAGCCATAGAGAACAAGCCCCATCCTGCGCCACCTGAGCCAACCTGAGCCACCTG TM
 31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L
 181 CTCATCATCGCCGACTGCTGATCGTCTGCTTGGCGGGCGTGACGGAGGGCCGCGGCATGCGCGCTCATGTTGAGGAGTCCGACACG
 61 L I I A G L L I V C L A G V T E G R R H A P L M F E E S D T
 271 GGCAGGCGGTCCAACCGACGAGCGGTACCGAATGCCAGTTTGGCAAAGTTTGGCGGAATTGGGGTCCACCTGGTATGCGGATTGGGT
 91 G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G
 361 CCACCCTTCGGAGTTATGTACTGCATCAAGTGTGAATGTGTGCGCATACCAAGAAGCGGCGCATCGTTGACGCGTCCAGTGTGCAAT
 121 P P F G V M Y C I K C E C V A I P K K R R I V A R V Q C R N CRI:W>A
 451 ATCAAAAACGAGTGGCCCGCGCCAAATGCCATGATCCCATCTCGTTGCCCGGAAATGCTGCAAGACCTGTCCCGCGGATCGAAACGAT
 151 I K N E C P P A K C D E F I S L P G K C C K T C P G D R N D
 541 ACGGATGTAGCCTTGGATGTGCCCCGTGCCAATGAGAGCAAGAGCGCAACATGAAACATTACGCTGCGTTGCTAACGGGCGGCACCTCC
 181 T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S
 631 TATTCCTCAAGGGTGAGGAAATGAAGTCCATGTACACCACCTACAATCCGCAGAATCTGGTGGCCACCGCCCGTTTCTGTTCACAAG
 211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K
 721 AAGAATCTATACTACTCCTTCTACACCTCATCGCAATCGGTGCTCCGCTGCCATTCAATTGTTGATGATGCGGGTGTAACTCTGGAG
 241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E
 811 GAGCATCAACTGGAGACCACCTTGGCGGGCACTCTCAGTGTCTATCAGAATGCCAGGGCAAGATCGGCGCGGCTCGAGGGGTACCTCTA
 271 E H Q L E T T L A G T L S V Y A N A T S K I G R G S R V P L pUAS Sequences
 901 GAGGATCTTTGTGAAGAACCTTACTTCTGTGTTGTGACATAATTGGACAAACTACCTACAGAGATTAAAGCTCTAA
 301 E D L C E G T L L L W C D I I G N T T Y R D L K L STOP

FIGURE 3

C cont'd

1 ATGGCCAAAGCTGAGGAAATCGAACGCCATCGAATGGGCCACGGCCACGGCCACAGTACCGCTCCTGGAAAGGAGCTGCTGCCACAGC
 1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S
 91 GAGGACGCGGCTGGAGCCCCAAGCGAGCAAAACCAGCCATAGAGAACAAGCCCCATCCTGCGCCACCTGAGCCAACTGAGCCACCTG TM
 31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L
 181 CTCATCATCGCGGACTGCTGATCGTCTGCTTGGCGGGCGTGACGGAGGGCGCGCGCATGCGCGCTCATGTTGAGGAGTCCGACAGC
 61 L I I A G L L I V C L A G V T E G R R H A P L M F E E S D T
 271 GGCAGGCGGTCCAACCGACAGCGGTCAACGAATGCCAGTTTGGCAAAGTTTGGCGGAATTGGGTCCACCTGGTATGCGGATTGGGT
 91 G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G
 361 CCACCCCTCGGAGTTATGTACTGCATCAAGTGTGAATGTGTGCGCATACCAAGAAGCGGCGCATCGTTGCACGCGTCCAGTGTGCAAT
 121 P P F G V M Y C I K C E C V A I P K K R R I V A R V Q C R N CRI
 451 ATCAAAAACGAGTGGCGCGCGCCAAATGCGATGATCGTCTCGTTGCCCGGAAATGCTGCAAGACCTGTCCGGGCGATCGAAACGAT
 151 I K N E C P P A K C D D P S L P G K C C K T C P G D R N D
 541 ACGGAITAGCCTTGGATGTGCGCGTGCCCAATGAAGAGCAAGCGCAACATGAAACATTACGCTGCGTTGCTAACGGGCGGCACCTCC
 181 T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S
 631 TATTTCCTCAAGGGTGAGGAAATGAAGTCCATGTACACCACCTACAATCGCAGAATCTGGTGGCCACCGCCGTTTCTGTTCACAAG
 211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K
 721 AAGAATCTATACTACTCTCTACACCTCATCGGAATCGGTCTGCGCGTGCATTCAATTGTTGATGATGCGGGTGTAATCCTGGAG
 241 K N L Y Y S F Y T S S R I G R P R A I O F V D D A G V I L E
 811 GAGCATCAACTGGAGACCACCTTGGCGGCACTCTCAGTGTCTATCAGAATGCCACGGCAAGATCGGCGCGGCTCGAGGCAGCGCGG
 271 E H Q L E T T L A G T L S V Y A N A T G K I G R G S R N R G PUAS/PCR
 901 CGCATCTTTTACCCATACGATGTTCTGACTATGCGGGCTATCCCTATCAGTCCCGGACTATGCAAGATCCTATCCATATGACCTTCCA
 301 R I F Y P Y D V F D Y A G Y P Y D V P D Y A G S Y P Y D V P SX-HA
 991 GATTACGCTGCTCAGTGGCGCGGATTATACGGACGACGACGACAAATCA IX-FLAG
 331 D Y A A N C G R D Y K D D D D K STOP

FIGURE 4

-351 ATATTAGATGGACATGCATAAATTATTCATGTAACATATGTGATTTTCATTTTACACGAGGTGTAAGTCAGAATTTAAATTTCTTAAAA
 -261 ATTGCAATCACGGCTTATTGTACATATTTATGTATGCGATCTCATTATTATTATTATTATTGATAATATATTAGCAGCTGTTCAAA
 -171 TCATCAACAAGTATAAAATTGAAAATGTTAAAAATGAAGCAGTCTTGGGTTTGCTGCAACATGTTGTGCGGATCGTTAGATGTTGCT

204 cDNA start

-81 GCTGCAATGTTGCCGTGTCATGTTGCCGTTGTCATGTTGCCGCGGTTTGCCAACTTTATAAACACGGAGCGGATTCAGTCCTTCAGGTTTCAG
 10 TCGCTCTTGAATTGCGTGGGATTGCACATCGGTCGTTTGGGTTTGGGTCGTCATTTAGAGAGATAGGATACGATCCGATACGATCCG
 100 ATCCAGTACAAAAATCAAATTCAAACCGCACTCCCGATCGGTCGTCATATACACGGCGGCTCGCACCGCAGCTATCTAGTAGATAA
 190 AAAGTCGCGGAGAACGCGATACGCATATAGCGAAACGCCAAAAAATAAAAAAAGTCGCGTTGCTTAATCCCTCCTCATACGAGAT
 280 CGACTCTATTTCCAGAGCAAGCTAAACACACTAGTGCTAAACCATAACTATATCTAACTAAGGAAACAAAGTCTCGAACTGAAAA
 370 CGAAAGCGCAATTTATGCGAGCCGCTAAATAAAAAACAGAAACCAAAACATAAAACACACTATACAAATCATACAAACAAAAACAGCGA
 460 ATCAAAATAGTATAAAAAAATAAATAAATGAGGAATAAAAAACAGGCAATAGAATAAATCCAATAAATCGGCGCGGAAACTCGCG
 550 TGTGTTATCTAATGTGCAAGAGAAGTACAAGAATCGGGTATAGAATCGGCTCTATACTATATCTATACACCTGATACTATATCCATT
 640 GTGTGTGCCAGTGTGTCGTTGGCGACCTTTGTTTTATATATTTTGTGTTGTTTCATCTGTGAAACGTGCTTTTACAAGCCGGTCG
 730 TTCAAAATACAAATACTACAAATCAAAATCAATCATATACACATACATATCAGTAAAAACAAAAACAAAAACACATAAACTGGCCAAC
 1 M A N

820 AAGCTGAGGAAATCGAAACCCATCGAATGGGCCACGGCCACCGGCACAGTACCGCTCCTGGAAAGGAGCTGCTGCCACAGCGAGGACGCC
 4 K L R K S N A I E W A T A T G T V P L L E R S C C H S E D A

910 GCACTGGAGCCCCAAGCGAGCAAAACCAGCCATAGAGAACAAGCCCCATCCTGCGCCACCTGAGCCAACTGAGCCACCTGCTCATCATC TM
 34 A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L L I I

1000 GCCGGACTGCTGATCGTCTGCTTGGGGGGCGTGACGGAGGGCGCGCGCATGCGCGCTCATGTTTCGAGGAGTCCGACACGGGCGAGCGCG
 64 A G L L I V C L A G V T E G R R H A P L M F E E S D T G R R

1090 TCCAACCGACCGCGCTCACCGAATGCCAGTTTGGCAAAGTTTGGCGCAATTGGGGTCCACCTGGTATGCGGATTGGGTCCACCCTTC
 94 S N R P A V T E C Q F R K V L R E L G S T W Y A D L G P P F

1180 GGAGTTATGTACTGCATCAAGTGTGAATGTGTGCGGATACCCAGAAGCGGCGCATCGTTGCACGCGTCCAGTGTGCGAATATCAAAAA
 124 G V M Y C I K C E C V A I P K K R R I V A R V Q C R N I K N

1270 GAGTGCCCGCGGCCAAATGCGATGATCCCATTTGCTTGGCCGAAATGCTGCAAGACCTGTCCCGCGGATCGAAACGATACCGATGTA
 154 E C P P A K C D D P I S A P G K C C K T C P S D R N D T D V

1360 GCCTTGGATGTGCCGTTGCCAATGAAGAGGAAGAGCGAACATGAACATTACGCTGCGTTGTAACGGGCGGACCTCCTATTTCCTC
 184 A L D V P V P N E E E E R N M K H Y A A L L T G R T S Y F L

1450 AAGGTGAGGAAATGAAGTCCATGTACACCACCTACAATCCGAGAATGTGGTGGCCACCGCCGTTTCTGTTCCACAAGAAGAACTCA
 214 K G E E M K S M Y T T Y N P C N V V A T A R F L F H K K N L

1540 TACTACTCCTTCTACACCTCATCGGAATCGGTCGTCGCGTGCATTCAATTCGTTGATGATGCGGGTGAATCCTGGAGGAGCATCA
 244 Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E E H Q

1630 CTGGAGACCACCTTGGCGGGCACTCTCAGTGTCTATCAGAATGCCACGGCAAGATCTGCGGTGTCTGGCGACGAGTTCACGTGATTAC
 274 L E T T L A G T L S V Y Q N A T G K I C G V W R R V P R D Y

1720 AAGCGCATCTGCGGACGATCGTCTCCATGTTGTCCTCTCTGGGCAACAAACAGCAGGCGGAGTTGGCTCTGGCCGGAAGGTGGCC
 304 K R I L R D D R L H V V L L W G N K Q Q A E L A L A G K V A

1810 AAATACACGGCCCTGCAGACGAGTTGTTTCAGTTTCGCTACTGGAGGCACCACTTCCCGATGGCAAAACGGATCCCAGCTGGCCGGAGCC
 334 K Y T A L Q T E L F S S L L E A P L P D G K T D P Q L A G A

1900 GGTGGCACAGCGATGTTGCCACGACGCGGTGCCCTCATCGATGCATCTCACCTCGTCTTCAATGGTGTCTTGGTGGCGAGGAG
 364 G G T A I V S T S S G A A S S M H L T D V F N G V F G A E E

1990 TACGCCGATGCAGCACTGAGTGTGAAAATTGAGCTGGCAGAACGGAAGGAGTGATCTTGATGAGATTCCACGTGTGCGCAACCCCTCT
 394 Y A D A A L S V K I E L A E R K E V I F D E I P R V R K P S

2080 GCCGAGATCAATGTCTGGAGTGTGTCGCGCCATTTCATACAGAATCTTCGACTGATGTCGCGTGGCAAACCTCTGCTGACCGTGGAG
 424 A E I N V L E L S S P I S I Q N L R L M S R G K L L L T V E

2170 TCCAAGAAGTACCCACATCTGCGCATCCAGGACACATCGTGACCCGAGCAGCTGCGAAATCTTCAGACCTGCTGCGCGCGCAGAT
 454 S K K Y P H L R I Q G H I V T R A S C E I F Q T L L A P H S

2260 GCCGAATCCTCGACCAAGAGCAGCGGTTTGGCGTGGGTCTACTTGAACACCGATGGATCTCTGGCCTACACATCGAAACGGAGCAGCTG SR1
 484 A E S S T K S S G L A W V Y L N T D G S L A Y N I E T E H V

2350 AACACCCGGGATAGGCCAACATCAGTTTGATTGAGGAGCAGGGCAAGCGGAAGCGCAAGCTGGAGGATCTGAGCGGAGCTTCAACTTC
 514 N T R D R P N I S L I E E Q G K R K A K L E D L T P S F N F

2440 AACAGGCCATTTGGTAGTGTGAGAAGTTGGGTCCCAAGTCTCGAGTCCGTGTATGCCGCGAACTGGCGGTTAATGTGGCCACCGAG
 544 N Q A I G S V E K L G P K V L E S L Y A G E L G V N V A T E

FIGURE 6

C control

CR1

FIGURE 1

Sub C

T M

CR1

PUAS
Sequences

Sub C

FIGURE 3

FIGURE 4 .

Sequence Range: 1 to 222

10 20 30 40 50 60 70
 Neg protel MERSQCLNTTPALMYFLGLRIDGGSCQHILHIFPAPSENPLVDLIEHPPTDPRKEDLNSTLRTLMVGHFDP
 SuperSog P 260 270 280
 (71) igfwddagvlla--EnqLettLagTlsV--yq
 Neg protel VDLIEHPPTDPRKEDLNSTLRTLMVGHFDP
 90 100 110 120 130 140 150
 Neg protel ILPEEPLGVEDLGEELMLPQKPSGMPAPKINGLETVEGLQSGHPLSLPLPPLQMWLWSQTTCFVLYTWNDLC
 SuperSog P 300 310
 (71) LrggsRwplDLcEgulllw
 Neg protel ILPEEPLGVEDLGEELMLR
 170 180 190 200 210 220
 Neg protel RYWRVGSCYSKPSGCVPEGMWCKAPASMLTILPWRCQPRVQKQWNTTIQYFTISECKCSC

Sub C

FIGURE 5

